



60 *
TGTGGGTTTCG AATTATTACCC ACCACAAGTT TTGTCCTACC ATAATTGGGA TAAGGAGTCT
120 *
AATTTCCTT GTACAATTTT CCAATTTCTT CCTCCGCCAC ACCATATATA TACTGTACGC
180 *
CACTTCGAAC GCTACAATGT TTGAAAAAAG ACGCAGATTT TACAAAGACG GAGAAGATAA
TAAGCTTCAA GTA CTCCGAT CGTCAGGTGG CCTTTGGAAG CCAACAAACT GGCT ATG
Met
240 *
GCT CTT TCT CTT CAC ACT GTA TTT CTC TGC AAA GAG GAA GCC CTC AAT
Ala Leu Ser Leu His Thr Val Phe Leu Cys Lys Glu Ala Leu Asn
300 *
TTA TAT GCA AGA TCA CCA TGT AAT GAA AGG TTT CAC AGG AGT GGA CAA
Leu Tyr Ala Arg Ser Pro Cys Asn Glu Arg Phe His Arg Ser Gly Gln
360 *
CCT CCT ACC AAC ATA ATC ATG ATG AAA ATT CGA TCC AAC AAT GGA TAT
Pro Pro Thr Asn Ile Ile Met Met Lys Ile Arg Ser Asn Asn Gly Tyr
420 *
TTT AAT TCT TTC CGG TTG TTT ACA TCT TAT AAG ACA AGT TCT TTC TCA
Phe Asn Ser Phe Arg Leu Phe Thr Ser Tyr Lys Thr Ser Ser Phe Ser

FIGURE 1A

GAT TCT AGC CAT TGC AAG GAT AAA TCT CAG ATA TGC AGC ATC GAT ACA
 Asp Ser Ser His Cys Lys Asp Lys Ser Gln Ile Cys Ser Ile Asp Thr

480
 *

AGT TTT GAG GAA ATA CAA AGA TTT GAT CTC AAA AGG GGC ATG ACT TTG
 Ser Phe Glu Glu Ile Gln Arg Phe Asp Leu Lys Arg Gly Met Thr Leu

540
 *

ATT CTT GAA AAG CAA TGG AGA CAA TTC ATA CAA TTG GCT ATC GTA TTG
 Ile Leu Glu Lys Gln Trp Arg Gln Phe Ile Gln Leu Ala Ile Val Leu

600
 *

GTT TGC ACA TTT GTT ATC GTT CCC AGA GTT GAT GCC GTT GAT GCT CTT
 Val Cys Thr Phe Val Ile Val Pro Arg Val Asp Ala Val Asp Ala Leu

660
 *

AAA ACT TGT GCT TGT TTA CTC AAA GAA TGC AGG ATT GAG CTT GCA AAA
 Lys Thr Cys Ala Cys Leu Leu Lys Glu Cys Arg Ile Glu Leu Ala Lys

TGT ATA GCA AAC CCA TCT TGT GCG GCA AAC GTT GCC TGT CTA CAG ACT
 Cys Ile Ala Asn Pro Ser Cys Ala Ala Asn Val Ala Cys Leu Gln Thr

720
 *

TGC AAC AAT CGT CCT GAC GAG ACC GAA TGT CAG ATA AAA TGT GGT GAC
 Cys Asn Asn Arg Pro Asp Glu Thr Glu Cys Gln Ile Lys Cys Gly Asp

FIGURE 1B

780 *
TTG TTC GAA AAC AGT GTG GTG GAC CAA TTC AAC GAG TGT GCG GTT TCC
Leu Phe Glu Asn Ser Val Val Asp Gln Phe Asn Glu Cys Ala Val Ser

840 *
CGA AAG AAA TGT GTG CCC CGG AAA TCG GAT GTG GGT GAA TTC CCG GTT
Arg Lys Lys Cys Val Pro Arg Lys Ser Asp Val Gly Glu Phe Pro Val

900 *
CCG GAT CGT AAT GCA GTG GTT CAA AAT TTT AAC ATG AAA GAC TTT AGT
Pro Asp Arg Asn Ala Val Val Gln Asn Phe Asn Met Lys Asp Phe Ser

960 *
GGG AAG TGG TAT ATA ACA AGT GGT TTA AAT CCT ACA TTT GAT GCA TTT
Gly Lys Trp Tyr Ile Thr Ser Gly Leu Asn Pro Thr Phe Asp Ala Phe

1020 *
GAT TGT CAA CTT CAT GAG TTT CAT ATG GAA AAT GAT AAA CTT GTT GGG
Asp Cys Gln Leu His Glu Phe His Met Glu Asn Asp Lys Leu Val Gly

1080 *
AAC TTA ACA TGG CGC ATA AAA ACT TTG GAT GGT GGT TTC TTT ACT CGA
Asn Leu Thr Trp Arg Ile Lys Thr Leu Asp Gly Gly Phe Thr Arg

1080 *
TCT GCT GTG CAA ACA TTT GTT CAA GAT CCA GAT CTT CCT GGA GCA CTT
Ser Ala Val Gln Thr Phe Val Gln Asp Pro Asp Leu Pro Gly Ala Leu

FIGURE 1C

1140 *

TAT AAT CAT GAC AAT GAG TTT CTT CAC TAC CAA GAT GAC TGG TAC ATA
Tyr Asn His Asp Asn Glu Phe Leu His Tyr Gln Asp Asp Trp Tyr Ile

TTA TCT TCC CAA ATC GAA AAC AAA CCC GAT GAT TAC ATA TTC GTA TAC
Leu Ser Ser Gln Ile Glu Asn Lys Pro Asp Asp Tyr Ile Phe Val Tyr

1200 *

TAC CGA GGT CGA AAC GAC GCA TGG GAT GGA TAC GGT GGG TCC GTG ATC
Tyr Arg Gly Arg Asn Asp Ala Trp Asp Gly Tyr Gly Ser Val Ile

1260 *

TAC ACC CGA AGC CCG ACA CTC CCC GAA TCG ATC ATC CCA AAC CTA CAA
Tyr Thr Arg Ser Pro Thr Leu Pro Glu Ser Ile Ile Pro Asn Leu Gln

1320 *

AAA GCA GCC AAA TCC GTG GGT CGA GAC TTT AAC AAT TTC ATA ACA ACC
Lys Ala Ala Lys Ser Val Gly Arg Asp Phe Asn Asn Phe Ile Thr Thr

1380 *

GAC AAT AGT TGT GGG CCT GAG CCT CCA TTG GTG GAA AGG CTT GAG AAA
Asp Asn Ser Cys Gly Pro Glu Pro Pro Leu Val Glu Arg Leu Glu Lys

ACA GCG GAA GAG GGC GAG AAG TTG TTG ATA AAA GAA GCT GTA GAG ATA
Thr Ala Glu Glu Gly Glu Lys Leu Leu Ile Lys Glu Ala Val Glu Ile

FIGURE 1D

1440
 *
 GAA GAA GAG GTT GAA AAA GAG GTG GAG AAG GTT AGA GAT ACT GAG ATG
 Glu Glu Glu Val Glu Lys Glu Val Glu Lys Val Arg Asp Thr Glu Met

 1500
 *
 ACT TTG TTT CAG AGG TTG CTT GAA GGG TTT AAG GAG TTG CAA CAA GAT
 Thr Leu Phe Gln Arg Leu Leu Glu Glu Phe Lys Glu Leu Gln Gln Asp

 1560
 *
 GAA GAG AAT TTT GTG AGG GAG TTG AGT AAA GAA GAG AAG GAA ATT CTG
 Glu Glu Asn Phe Val Arg Glu Glu Leu Ser Lys Glu Lys Glu Ile Leu

 1620
 *
 AAT GAA CTT CAA ATG GAA GCG ACT GAA GTT GAA AAG CTT TTT GGG CGC
 Asn Glu Leu Gln Met Glu Ala Thr Glu Val Glu Lys Leu Phe Gly Arg

 1680
 *
 GCG TTA CCG ATT AGG AAA CTT AGA TAAATTT CGATGATTGA TTCAGACAAT
 Ala Leu Pro Ile Arg Lys Leu Arg

 1740
 *
 ATATATAGTC ATATGGATTA TGTAGATACT AGAGAAAACC CAAAAAAACT TTTGTATACG

 1800
 *
 TGATAAACGT GTTTGTGATT TGTTTATTGG CTTAAAAATTG TAGAATAGCT TTTTAAATTC

FIGURE 1E

1860

*

TTTACAAAAA AATTGATTGT CTATTGGTAG CCAAGAGGTT CACGAAAAGA CTGAAAGGGT

1920

*

CTTGCCGGT TTGCGGGTTA GGCCAAATTT TTTGGGGCGG GATCGGTCIT GATCGGGTTTT

1980

*

TCCTTAAAA CATGTATTTT TTATAAATGA TGAGTTATTT TCAATTTTIG GCTAAAAAAA

1981

*

A

FIGURE 1F

TATTTTCATG AGTTTGCAGT TGGTGGTAAT ACGGTTGAAG A ATG GCT CTT GCC
CCT

M A L A

P

60

*

CAT TCA AAT TTT CTG GCC AAC CAT GAA ACC ATC AAA TAT TAT GTT

GGG

H S N F L A N H E T I K Y Y V G

120

*

TCA AAG CTT CCC GGT CAT AAA AGG TTT AGC TGG GGT TGG GAA GAT

TAC

S K L P G H K R F S W G W E D Y

180

*

TTT GGT AGT ATA GTC GTA GCA AAA ATT TGT TCC AGC AGA CGG ATA

CCT

F G S I V V A K I C S S R R I P

240

*

AGA TAC TTT CGA AAA TCT CCT AGA ATA TGC TGT GGT TTG GAT TCA

AGA

R Y F R K S P R I C C G L D S R

GGT CTG CAA CTA TTC TCA CAC GGG AAA CAC AAT CTC TCT CCC GCA

CAT

G L Q L F S H G K H N L S P A H

300

*

AGC ATT AAC CAG AAT GTA CCT AAG GGA AAT TCA GGA TGC AAA TTT

CCA

S I N Q N V P K G N S G C K F P

360

*

AAA GAT GTA GCT TTG ATG GTT TGG GAG AAA TGG GGC CAA TTT GCC

AAA

K D V A L M V W E K W G Q F A K

420

*

ACA GCA ATT GTA GCT ATA TTC ATT TTG TCA GTT GCT TCA AAA GCT

GAT

T A I V A I F I L S V A S K A D

480

*

GCG GTT GAT GCT CTC AAG ACT TGT ACT TGC TTA CTG AAA GAG TGC

AGG

FIGURE 2A

A V D A L K T C T C L L K E C R
 TTA GAG CTT GCG AAG TGC ATT TCG AAC CCT GCA TGT GCA GCT AAT
 GTT
 L E L A K C I S N P A C A A N V
 540
 *
 GCC TGT CTC CAG ACT TGC AAC AAT AGA CCT GAC GAA ACG GAA TGT
 CAG
 A C L Q T C N N R P D E T E C Q
 600
 *
 ATA AAA TGT GGT GAT TTG TTT GAA AAC AGT GTC GTA GAC GAG TTC
 AAT
 I K C G D L F E N S V V D E F N
 660
 *
 GAG TGT GCA GTC TCC CGA AAG AAA TGT GTA CCT CGT AAA TCT GAT
 GTT
 E C A V S R K K C V P R K S D V
 720
 *
 GGT GAC TTT CCT GTA CCT GAT CCC AGT GTT CTT GTC CAG AAG TTT
 GAC
 G D F P V P D P S V L V Q K F D
 ATG AAA GAT TTT AGC GGG AAA TGG TTC ATT ACT CGC GGT TTG AAT
 CCC
 M K D F S G K W F I T R G L N P
 780
 *
 ACT TTT GAT GCT TTT GAT TGC CAA TTG CAT GAG TTC CAT ACA GAA
 GAA
 T F D A F D C Q L H E F H T E E
 840
 *
 AAC AAA CTT GTG GGG AAT TTA TCT TGG AGA ATA CGT ACA CCT GAT
 GGA
 N K L V G N L S W R I R T P D G
 900
 *
 GGA TTT TTT ACT CGA TCA GCG GTG CAA AAA TTC GTG CAA GAT CCA
 AAG
 G F F T R S A V Q K F V Q D P K
 960
 *

FIGURE 2B

TAT CCG GGG ATA CTC TAC AAT CAT GAT AAT GAG TAT CTT CTC TAC
 CAA
 Y P G I L Y N H D N E Y L L Y Q

GAT GAC TGG TAT ATT TTG TCA TCC AAA GTA GAA AAT AGT CCA GAG
 GAT
 D D W Y I L S S K V E N S P E

1020

*

TAC ATA TTT GTG TAC TAT AAG GGC AGA AAT GAT GCA TGG GAT GGA
 TAT
 Y I F V Y Y K G R N D A W D G Y

1080

*

GGT GGT TCT GTA CTT TAC ACA AGA AGT GCA GTT TTG CCT GAA AGC
 ATT
 G G S V L Y T R S A V L P E S I

1140

*

ATA CCG GAG TTG CAA ACC GCA GCT CAA AAA GTT GGG CGT GAT TTC
 AAC
 I P E L Q T A A Q K V G R D F N

1200

*

ACA TTC ATA AAA ACA GAC AAT ACA TGT GGC CCT GAA CCT CCC CTT
 GTT
 T F I K T D N T C G P E P P L V

GAG AGG TTG GAG AAG AAA GTG GAA GAA GGA GAA AGG ACG ATC ATA
 AAA
 E R L E K K V E E G E R T I I K

1260

*

GAA GTT GAG GAG ATA GAA GAA GAA GTA GAG AAG GTG AGA GAT AAA
 GAA
 E V E E I E E E V E K V R D K E

1320

*

GTC ACC TTA TTC AGT AAA CTG TTT GAA GGT TTT AAA GAG CTC CAA
 CGA
 V T L F S K L F E G F K E L Q R

1380

*

GAT GAA GAG AAC TTC TTA AGA GAG CTG AGC AAA GAA GAA ATG GAT
 GTT
 D E E N F L R E L S K E E M D V

1440

FIGURE 2C

TTG GAT GGA CTT AAA ATG GAA GCA ACT GAG GTA GAA AAA CTT TTT

GGG

L D G L K M E A T E V E K L F G

1500

*

CGT GCT TTA CCA ATA AGG AAA TTA A GGTAAGT ATTTTAAAA
CTATCAACAT

R A L P I R K L X

1560

*

ATATACTACA TGTATAGTTG TATTTGATTC TTTTGCCTGG AATAGATTGC

TTATACATCA TGTATTGCTT CTTTTTCAGA AGCAAAAAA

FIGURE 2D

CCACGCGTCC GGCTTGGTGT GGGGAAGATT AGATAGTGTG A AGA ATG GCA GTA GCT
R M A V A

60

*

ACA CAT TGT TTC ACT TCA CCT TGT CAT GAC CGT ATT CGA TTT TTC TCA
T H C F T S P C H D R I R F F S

120

*

AGT GAT GAT GGT ATT GGT AGG CTT GGC ATT ACA AGA AAG AGG ATC AAT
S D D G I G R L G I T R K R I N

180

*

GGC ACT TTC TTG CTC AAG ATT TTA CCT CCA ATC CAA AGT GCT GAT CTC
G T F L L K I L P P I Q S A D L

240

*

AGA ACA ACT GGT GGG AGA TCC TCA CGT CCT TTA TCT GCA TTC AGG TCA
R T T G G R S S R P L S A F R S

GGA TTC TCT AAG GGG ATA TTT GAC ATT GTG CCA TTA CCA TCA AAG AAT
G F S K G I F D I V P L P S K N

300

*

GAG CTG AAA GAG CTG ACC GCT CCG CTG TTG CTA AAA CTC GTG GGT GTT
E L K E L T A P L L L K L V G V

360

*

TTA GCT TGC GCG TTC CTT ATT GTT CCA TCT GCA GAT GCA GTT GAT GCA
L A C A F L I V P S A D A V D A

420

*

CTT AAA ACT TGT GCA TGC TTA TTG AAG GGA TGC AGG ATA GAA CTC GCA
L K T C A C L L K G C R I E L A

480

*

AAG TGC ATT GCC AAC CCT GCC TGT GCA GCC AAT GTC GCG TGC CTT CAG
K C I A N P A C A A N V A C L Q

ACC TGC AAT AAC CGT CCA GAT GAA ACC GAG TGC CAG ATT AAA TGT GGG
T C N N R P D E T E C Q I K C G

540

*

GAT CTG TTT GAG AAC AGT GTT GTT GAT GAG TTC AAC GAG TGT GCT GTG
D L F E N S V V D E F N E C A V

600

FIGURE 3A

*

TCG AGA AAA AAG TGT GTT CCT AGA AAA TCT GAT CTC GGA GAA TTT CCT
 S R K K C V P R K S D L G E F P

660

*

GCC CCA GAC CCT TCT GTT CTT GTA CAG AAC TTC AAC ATC TCG GAC TTT
 A P D P S V L V Q N F N I S D E

720

*

AAC GGG AAG TGG TAC ATT ACA AGT GGC TTG AAT CCA ACC TTT GAT GCC
 N G K W Y I T S G L N P T F D A

TTC GAC TGC CAG CTG CAT GAG TTC CAC ACA GAA GGT GAC AAC AAG CTT
 F D C Q L H E F H T E G D N K L

780

*

GTT GGA AAC ATC TCT TGG AGA ATA AAG ACC CTA GAC AGT GGA TTC TTT
 V G N I S W R I K T L D S G F F

840

*

ACT AGG TCA GCC GTA CAA AAA TTC GTG CAA GAT CCT AAC CAA CCT GGT
 T R S A V Q K F V Q D P N Q P G

900

*

GTT CTC TAC AAT CAT GAC AAC GAG TAC CTT CAC TAT CAA GAT GAC TGG
 V L Y N H D N E Y L H Y Q D D W

960

*

TAT ATC CTG TCA TCA AAG ATA GAG AAT AAA CCT GAA GAC TAT ATA TTT
 Y I L S S K I E N K P E D Y I F

GTA TAC TAC CGT GGG CGA AAC GAT GCT TGG GAT GGA TAT GGT GGT GCA
 V Y Y R G R N D A W D G Y G G A

1020

*

GTT GTA TAC ACG AGA AGT TCT GTA TTA CCC AAT AGC ATT ATA CCA GAA
 V V Y T R S S V L P N S I I P E

1080

*

CTC GAA AAA GCA GCA AAA AGC ATA GGC AGA GAC TTC AGC ACA TTC ATT
 L E K A A K S I G R D F S T F I

1140

*

AGA ACG GAT AAC ACA TGT GGT CCT GAA CCT GCG CTC GTG GAG AGA ATT
 R T D N T C G P E P A L V E R I

FIGURE 3B

1200

GAG AAG ACA GTG GAA GAA GGT GAA AGG ATA ATC GTA AAA GAG GTT GAA
E K T V E E G E R I I V K E V E

GAG ATA GAA GAA GAG GTA GAG AAG GAA GTG GAG AAG GTC GGT AGG ACT
E I E E E V E K E V E K V G R T

1260

*

GAG ATG ACC TTG TTC CAG AGA TTG GCT GAA GGA TTT AAT GAA CTG AAG
E M T L F Q R L A E G F N E L K

1320

*

CAA GAC GAG GAG AAT TTC GTG AGA GAG TTA AGT AAA GAA GAG ATG GAG
Q D E E N F V R E L S K E E M E

1380

*

TTT TTG GAT GAG ATC AAA ATG GAA GCA AGT GAG GTT GAA AAA TTG TTT
F L D E I K M E A S E V E K L F

1440

*

GGG AAA GCT TTG CCA ATC AGG AAG GTC A GG TAGAAACAAG AACCACCATT
G K A L P I R K V X

1500

*

GTTGTACAAA CTATATTATA CATACTGTGT TCGGTTTCATA TAAAGTAATA TTTTGTACA
CAGTCATCAT CATTCCATAA CAATTGGATA AAAAAAAAAA AAAAA

FIGURE 3C



- A Cysteine-rich domain
- B Lipocalin signature
- C Highly charged domain

FIGURE 4A

Tobacco	MALAPHSNFLANHETIKYYVGSKLPGHKRFSWGWEDYFGSIVVAKICSSR	50
Arabidopsis	M-V-T-.....CFT-PCHDRI--FSS.D-GI-RLGITRK....	33
Lettuce	M--SL-TV--CKE-ALNL-AR-PCNE...--HRS.GQPPTN-IMM--....	43
Tobacco	RIPRYFRKSPRICCGLDSEGLQLF.SHGKHNLSPAHSINQNVPKGNSGCK	99
Arabidopsis	--NGT-L..LK-LPPIQ-AD-RTTGGRSSRP--AFR-GFSKGIFDIVPLP	81
Lettuce	-SNNGYFN-F-LFTSYKTSSF..SD-SHCKDK-QI.CSIDTSFEEIQRFD	90
Tobacco	FPKDVALMVWEKVGQFAKTAIVAIFILSVASKADA	134
Arabidopsis	SKNELKELTA...PLLL-LVG-LACAFILVPS---	113
Lettuce	LKRGMT-ILEKQ-R--IQL---LVCTFVIVPRV--	125
Tobacco	VDALKTCTCLLKECRLELAKCISNPACAAVACLQTCNNRPDETECQIKC	50
Arabidopsis	-----A---G---I-----A-----	50
Lettuce	-----A-----I-----A--S-----	50
Tobacco	GDLFENSVVDEFNECAVSRKKCVPRKSDVGFVPDPSPVLVQKFDMDKDFS	100
Arabidopsis	-----L-E--A-----N-NIS--N	100
Lettuce	-----Q-----E-----RNAV--N-N-----	100
Tobacco	GKWFITRGLNPTFADFDCQLHEFHTE.ENKLVGNLSWRIRTPDGGFFTRS	149
Arabidopsis	---Y--S-----GD-----I---K-L-S-----	150
Lettuce	---Y--S-----M-ND.-----T---K-L-----	149
Tobacco	AVQKFVQDPKYPGILYNHDNEYLLYQDDWYILSSKVENSPEDYIFVYYKG	199
Arabidopsis	-----NQ--V-----H-----I--K-----R-	200
Lettuce	---T---DL--A-----F-H-----QI--K-D-----R-	199
Tobacco	RNDADWDGYGGSVLVYTRSAVLPESIPELQTAAQKVGRDENTFIKTDNTCG	249
Arabidopsis	-----A-V-----S---N-----EK--KSI---S---R-----	250
Lettuce	-----I---PT-----N--K--KS-----N--T---S--	249
Tobacco	PEPPLVERLEKKVEEGERTIIKEVEEIEE...EVEKVRDKEVTLFSKLF	295
Arabidopsis	---A---I--T-----I-V-----EVEK-----GRT-M---QR-A	300
Lettuce	-----TA---KLL---AV---EVEK-----T-M---QR-L	299
Tobacco	EGFKELQRDEENFLRELSKEEMDVLGDKMEATEVEKLFGRALPIRKLR	344
Arabidopsis	---N--KQ-----V-----EF--EI---S-----K-----V-	349
Lettuce	-----Q-----V-----KEI-NE-Q-----	348

FIGURE 4B

Percent Identity and Similarity* of Pre-protein VDE

	Lettuce	Tobacco	Arabidopsis
Lettuce		67 (78)	69 (82)
Tobacco	69	<i>protein</i> <i>cDNA</i>	68 (81)
Arabidopsis	66	68	

*similarity values are in parentheses

Percent Identity and Similarity* of Mature VDE

	Lettuce	Tobacco	Arabidopsis
Lettuce		82 (90)	83 (91)
Tobacco	76	<i>protein</i> <i>cDNA</i>	83 (92)
Arabidopsis	74	77	

*similarity values are in parentheses

FIGURE 5

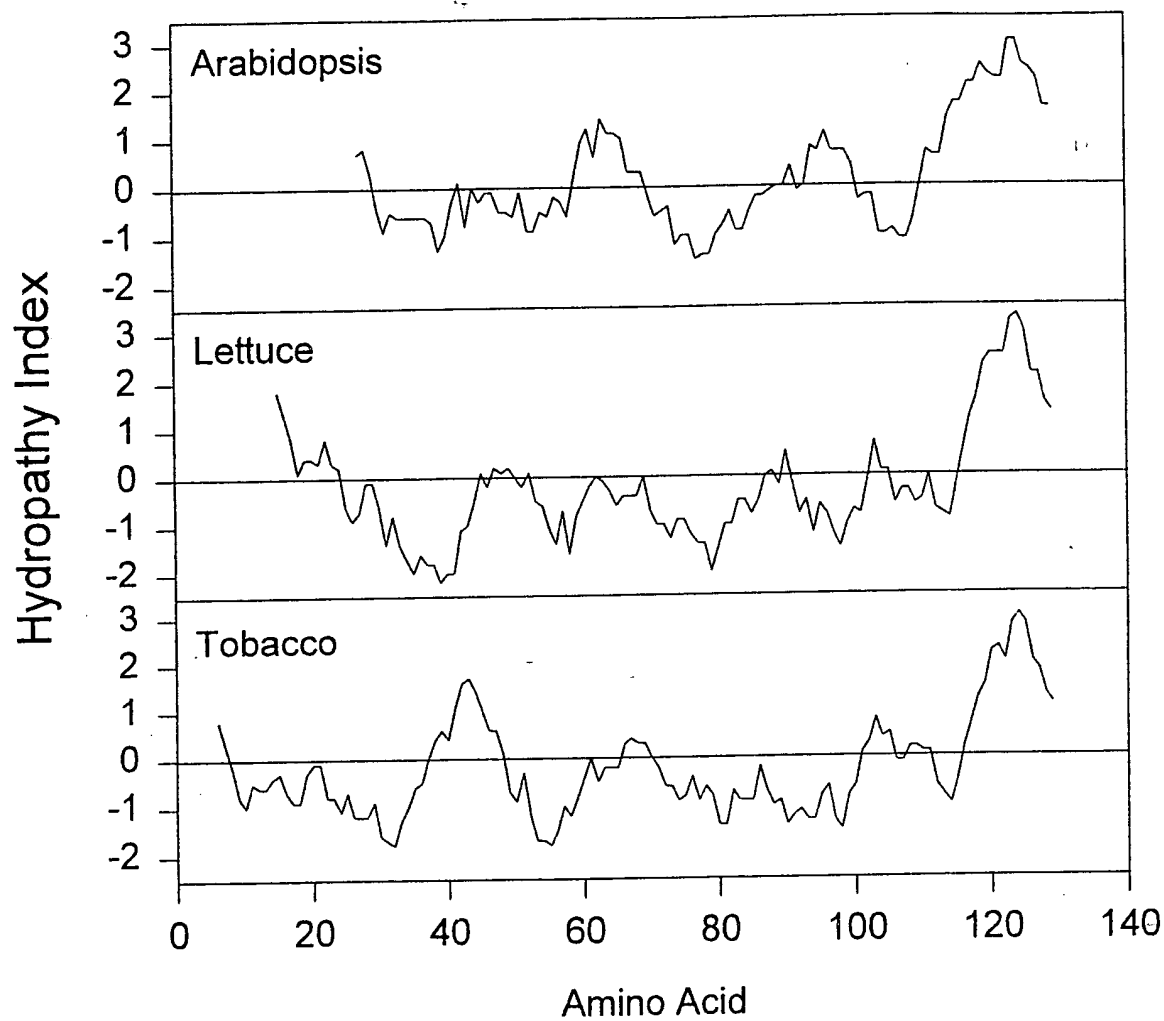


FIGURE 6

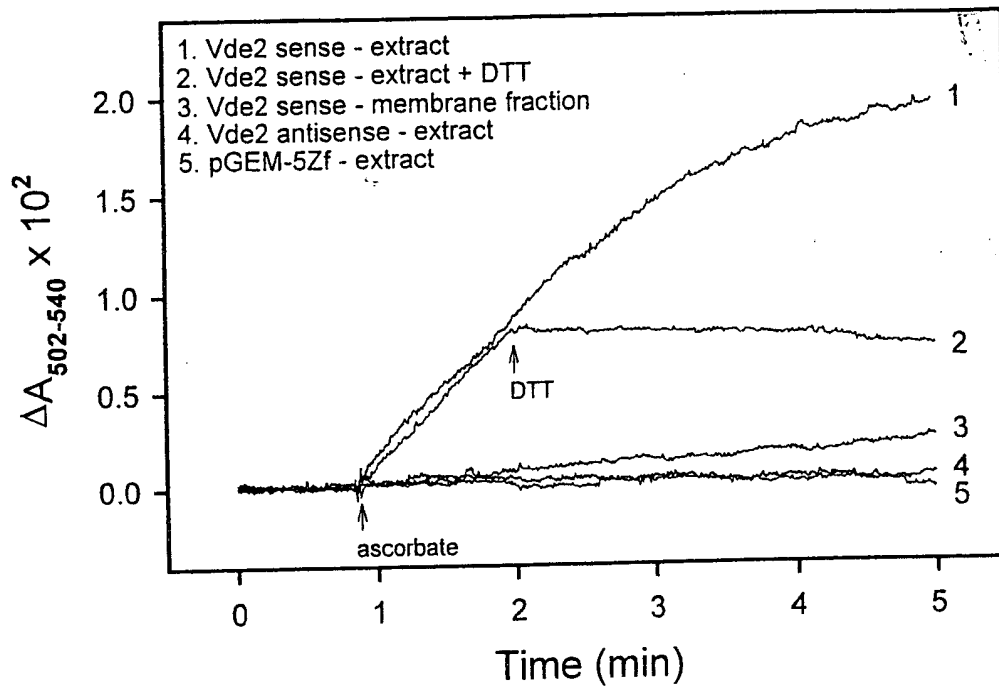


FIGURE 7B

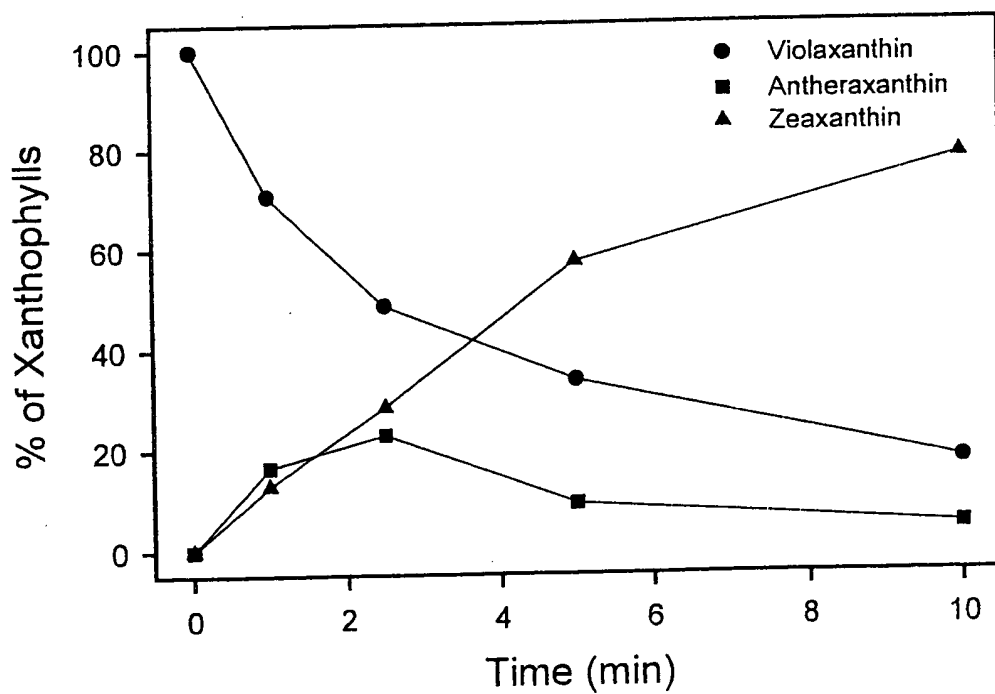


FIGURE 7A

Plant	Treatment	N	V	A	Z	V+A+Z	L	Chlb/Chla	$\beta\beta$ -Carotene	%V Deepoxidized
Ct-11	Dark	77.13	64.67	1.54	0	66.21	335.12	0.39	136.95	60.5
	Light	77.65	25.56	6.25	30.93	62.74	338.15	0.40	131.76	
Ct-14	Dark	71.60	77.74	1.19	0	78.93	312.05	0.36	150.08	62.6
	Light	72.00	29.07	7.97	43.07	80.11	311.36	0.37	151.50	
Ct-15	Dark	76.68	67.44	0	0	67.44	345.73	0.43	130.05	60.4
	Light	74.45	26.73	7.78	37.44	71.95	337.87	0.42	126.36	
Ct-18	Dark	68.28	82.55	2.33	0	84.88	298.36	0.35	136.67	58.2
	Light	69.65	34.50	13.25	38.44	86.19	311.07	0.36	138.95	
Ct-20	Dark	78.45	70.60	2.85	0	73.45	351.57	0.39	139.58	67.2
	Light	77.38	23.14	5.46	42.66	71.26	343.25	0.39	133.61	
Ct-22	Dark	72.68	104.14	3.40	0	107.54	323.93	0.37	138.29	73.5
	Light	72.13	27.63	6.62	78.66	112.91	315.07	0.40	128.30	
Ct-24	Dark	70.77	76.82	1.55	0	78.37	334.20	0.43	132.95	61.8
	Light	76.52	29.35	7.92	45.24	82.51	339.60	0.44	131.55	
Ct-26	Dark	75.28	63.41	0	0	63.41	346.45	0.44	130.38	58.6
	Light	77.34	26.27	6.16	34.19	66.62	346.91	0.44	128.27	
Ct-30	Dark	78.23	59.66	1.73	0	61.39	357.63	0.45	127.62	55.6
	Light	79.37	26.47	4.93	31.61	63.01	352.39	0.46	124.80	
Ct-31	Dark	71.72	75.91	1.74	0	77.65	315.40	0.37	144.24	58.6
	Light	73.00	31.43	8.74	37.65	77.82	312.80	0.38	145.13	
Ct-39	Dark	75.99	77.93	0	0	77.93	335.79	0.43	127.17	66.3
	Light	74.79	26.28	8.07	41.30	75.65	331.35	0.42	123.11	
Ct-40	Dark	77.56	79.07	2.99	0	82.06	358.33	0.44	128.05	65.3
	Light	77.78	27.44	10.10	47.92	85.46	352.66	0.43	120.89	

N = 9'-cis-neoxanthin V = violaxanthin A = antheraxanthin Z = zeaxanthin L = lutein Chla = chlorophyll a Chlb = chlorophyll b
 All values are relative to chlorophyll a (mmol mol⁻¹ Chla) except Chlb/Chla which is (mol/mol).

Mean = 62.4 ± 5.0

FIGURE 8A

Plant	Treatment	N	V	A	Z	V+A+Z	L	Chlb/Chla	ββ-Carotene	%V De-epoxidized	% Inhibition of De-epoxidation
TAS-32	Dark	74.19	76.98	0	0	76.98	325.75	0.42	136.45		
	Light	73.78	74.15	2.18	0	76.33	330.95	0.41	131.73	3.7	94.1
TAS-39	Dark	77.92	59.19	0	0	59.19	329.29	0.41	141.45		
	Light	75.06	56.39	2.70	0	59.09	322.29	0.40	141.52	4.7	92.5
TAS-21	Dark	75.78	53.19	0	0	53.19	335.21	0.45	132.85		
	Light	77.92	43.90	7.30	9.37	60.57	326.90	0.45	130.33	17.5	72.0
TAS-5	Dark	67.82	79.21	3.43	0	82.64	300.82	0.39	139.00		
	Light	69.72	62.31	14.66	8.27	85.24	300.63	0.40	137.13	21.3	65.9
TAS-17	Dark	74.89	64.54	1.08	0	65.62	317.69	0.41	143.42		
	Light	74.00	49.89	8.49	8.53	66.91	325.32	0.40	139.28	22.7	63.6
TAS-13	Dark	77.92	49.33	1.27	0	50.60	339.63	0.45	135.36		
	Light	78.02	37.82	4.94	7.18	49.94	340.45	0.45	132.78	23.3	62.7
TAS-6	Dark	74.42	55.77	0	0	55.77	340.84	0.44	136.77		
	Light	74.95	40.27	9.69	13.99	63.95	332.00	0.44	135.36	27.8	55.4
TAS-37	Dark	73.05	59.18	1.24	0	60.42	323.30	0.39	135.81		
	Light	71.36	38.97	14.48	9.98	63.43	313.46	0.38	134.62	34.1	45.3
TAS-3	Dark	74.04	60.25	1.76	0	62.01	319.39	0.43	138.89		
	Light	76.98	39.26	7.41	14.33	61.00	322.14	0.44	136.00	34.8	44.2
TAS-36	Dark	69.77	77.86	1.42	0	79.28	295.52	0.36	151.33		
	Light	70.74	48.73	12.76	12.81	74.30	308.06	0.36	151.35	37.4	40.1
TAS-35	Dark	75.59	63.24	1.05	0	64.29	342.09	0.42	130.30		
	Light	75.76	39.48	10.38	17.49	67.35	337.57	0.42	128.88	37.6	39.7
TAS-4	Dark	73.61	68.23	1.31	0	69.54	321.12	0.42	135.43		
	Light	73.23	42.07	8.95	17.84	68.86	320.33	0.42	131.73	38.3	38.6
TAS-9	Dark	72.28	52.57	1.75	0	54.32	324.02	0.42	140.21		
	Light	73.28	31.72	6.19	18.59	56.50	317.11	0.42	136.93	39.7	36.4
TAS-7	Dark	72.55	71.02	1.81	0	72.83	321.37	0.40	133.21		

FIGURE 8B

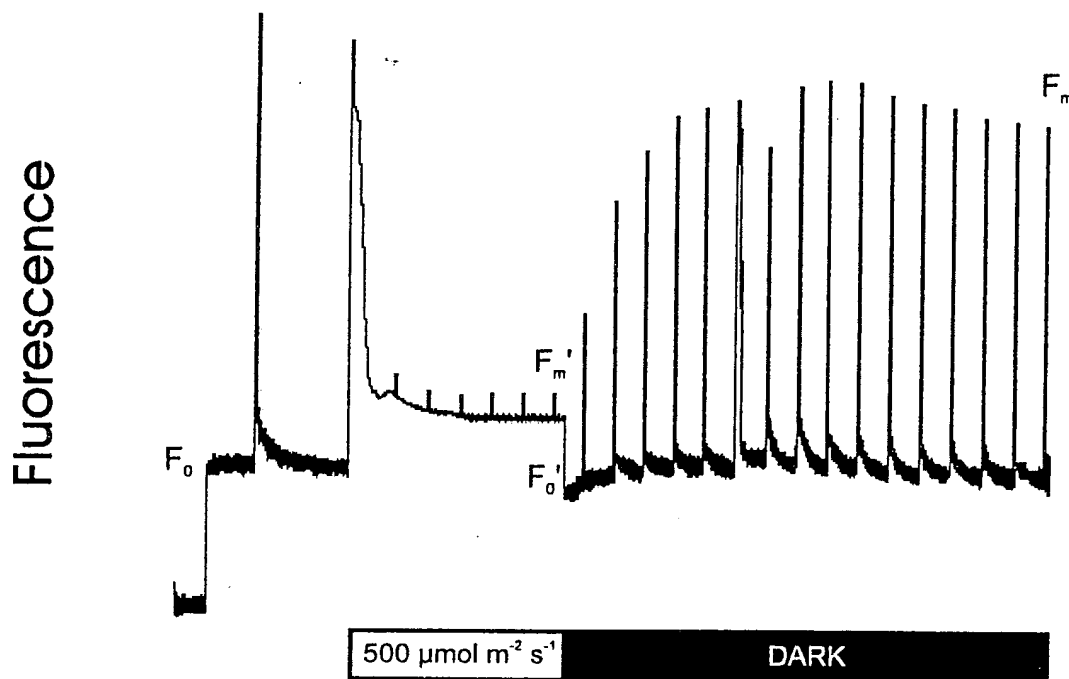
	Light	71.79	39.82	14.04	21.09	74.95	322.04	0.40	130.57	43.9	29.6
TAS-38	Dark	71.66	61.97	1.77	0	63.74	329.67	0.41	135.87		
	Light	73.24	34.45	8.83	19.57	62.85	331.17	0.41	133.77	44.4	28.8
TAS-16	Dark	72.15	62.54	2.04	0	64.58	329.72	0.41	135.12		
	Light	74.04	33.28	9.10	23.83	66.21	335.60	0.42	131.32	46.8	25.0
TAS-18	Dark	75.09	59.64	1.72	0	61.36	345.04	0.42	127.38		
	Light	75.26	31.68	7.11	23.01	61.80	340.79	0.42	126.85	46.9	24.8
TAS-34	Dark	72.35	65.39	1.79	0	67.18	326.06	0.41	131.12		
	Light	71.25	34.26	9.26	30.41	73.93	316.49	0.42	128.96	47.6	23.7

N = 9'-cis-neoxanthin V = violaxanthin A = antheraxanthin Z = zeaxanthin L = lutein Chla = chlorophyll a Chlb = chlorophyll b

All values are relative to chlorophyll a (mmol mol⁻¹ Chla) except Chlb/Chla which is (mol/mol).

FIGURE 8C

Ct-30

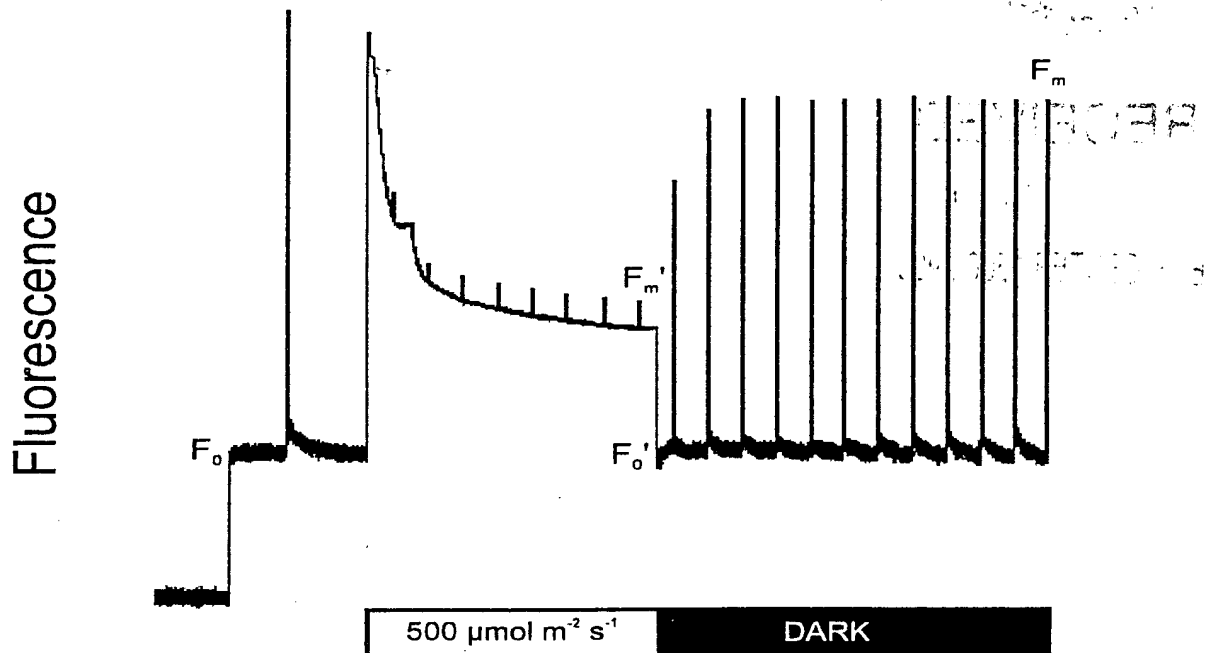


	Dark-adapted	Pre-illuminated	Post-fluorescence Analysis
V	64.28	51.77	44.98
A	1.99	6.16	11.10
Z	0	10.17	13.77
V+A+Z	66.27	68.10	69.85
De-epoxidation (%)		19.5	30.00
(F _m /F _{m'}) - 1			2.20
(F _o /F _{o'}) - 1			0.15

All values are relative to chlorophyll *a* ($\text{mmol mol}^{-1} \text{Chla}$).

FIGURE 9

TAS-5



	Dark-adapted	Pre-illuminated	Post-fluorescence Analysis
V	67.51	NA	65.38
A	0	NA	2.14
Z	0	NA	0
V+A+Z	67.51	NA	67.52
De-epoxidation (%)		NA	3.20
(Fm/Fm') - 1			1.34
(Fo/Fo') - 1			0

All values are relative to chlorophyll a ($\text{mmol mol}^{-1} \text{Chla}$).

NA - Not assayed

FIGURE 10